

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/811,045A

DATE: 06/29/2001

TIME: 12:17:00

Input Set : A:\D6386D_SEQ.txt

Output Set: N:\CRF3\06292001\I811045A.raw

ENTERED

2 <110> APPLICANT: Scott, Robert E.
 4 <120> TITLE OF INVENTION: cDNA encoding P2P proteins and use of P2P cDNA-
 5 derived antibodies and antisense reagents
 6 in determining the proliferative potential of
 7 normal, abnormal and cancer cells in animals
 8 and humans
 10 <130> FILE REFERENCE: D6386D
 12 <140> CURRENT APPLICATION NUMBER: US 09/811,045A
 13 <141> CURRENT FILING DATE: 2001-03-16
 14 <150> PRIOR APPLICATION NUMBER: US 08/801,308
 15 <151> PRIOR FILING DATE: 1997-02-18
 17 <160> NUMBER OF SEQ ID NOS: 4
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1404
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Unknown
 24 <220> FEATURE:
 26 <221> NAME/KEY: PEPTIDE
 27 <223> OTHER INFORMATION: P2P polypeptide
 29 <400> SEQUENCE: 1
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 31 5 10 15
 32 Asn Thr Gly Lys Tyr Ala Ile Pro Thr Ile Asp Ala Glu Ala Tyr
 33 20 25 30
 34 Ala Ile Gly Lys Lys Glu Lys Pro Pro Phe Leu Pro Glu Glu Pro
 35 35 40 45
 36 Ser Ser Ser Ser Glu Glu Asp Asp Pro Ile Pro Ala Glu Leu Leu
 37 50 55 60
 38 Cys Leu Ile Cys Lys Asp Ile Met Thr Asp Ala Val Val Ile Pro
 39 65 70 75
 40 Cys Cys Gly Asn Ser Ser Cys Asp Glu Cys Ile Arg Thr Thr Leu
 41 80 85 90
 42 Leu Glu Ser Asp Lys His Thr Cys Pro Thr Cys His Gln Asn Asp
 43 95 100 105
 44 Val Ser Pro Asp Ala Leu Ile Ala Asn Lys Phe Leu Arg Gln Ala
 45 110 115 120
 46 Val Asn Asn Phe Lys Asn Glu Thr Gly Tyr Thr Lys Arg Leu Arg
 47 125 130 135
 48 Lys Gln Leu Pro Pro Phe Leu Phe Leu Val Pro Pro Pro Arg Pro
 49 140 145 150
 50 Leu Ser Gln Arg Asn Leu Gln Pro Arg Ser Arg Ser Pro Ile Leu
 51 155 160 165
 52 Arg Gln Gln Asp Pro Val Val Phe Arg Tyr Thr Val Ser Pro Thr
 53 170 175 180
 54 Cys Ser Asp Thr Lys Thr Ala Gly Ser Cys Ser Asp Ser Gly Thr
 55 185 190 195
 56 Leu Ser Arg Leu Pro Ala Pro Ser Ile Ser Ser Leu Thr Ser Asn

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59		215		220		225
60	Pro Ala Pro Val	Pro Asp Ile Thr Ala	Thr Val Ser Ile Ser	Val		
61		230		235		240
62	His Ser Glu Lys	Ser Asp Gly Pro Phe	Arg Asp Ser Asp Asn	Lys		
63		245		250		255
64	Leu Leu Pro Ala	Ala Ala Leu Thr Ser	Glu His Ser Lys Gly	Ala		
65		260		265		270
66	Ser Ser Ile Ala	Ile Thr Ala Leu Met	Glu Glu Lys Gly Val	Pro		
67		275		280		285
68	Gly Thr Ser Pro	Trp Asn Ser Ile Phe	Val Gly Gln Ser Leu	Leu		
69		290		295		300
70	His Gly Gln Leu	Ile Pro Thr Thr Gly	Pro Val Arg Ile Asn	Ala		
71		305		310		315
72	Ala Arg Pro Gly	Gly Gly Arg Pro Gly	Trp Glu His Ser Asn	Lys		
73		320		325		330
74	Leu Gly Tyr Leu	Val Ser Pro Pro Gln	Gln Ile Arg Arg Gly	Glu		
75		335		340		345
76	Arg Ser Cys Tyr	Arg Ser Ile Asn Arg	Gly Arg His His Ser	Glu		
77		350		355		360
78	Arg Ser Gln Arg	Thr Gln Ser Pro Ser	Leu Pro Ala Thr Pro	Cys		
79		365		370		375
80	Phe Val Pro Val	Pro Pro Pro Pro Leu	Tyr Pro Pro Pro Pro	His		
81		380		385		390
82	Thr Leu Pro Leu	Pro Pro Gly Val Pro	Pro Pro Gln Phe Ser	Pro		
83		395		400		405
84	Gln Phe Pro Ser	Ser Gln Pro Pro Thr	Ala Gly Tyr Ser Val	Pro		
85		410		415		420
86	Pro Pro Gly Phe	Pro Pro Ala Pro Ala	Asn Ile Ser Thr Ala	Cys		
87		425		430		435
88	Phe Ser Pro Gly	Val Pro Thr Ala His	Ser Asn Thr Met Pro	Thr		
89		440		445		450
90	Thr Gln Ala Pro	Leu Leu Ser Arg Glu	Glu Phe Tyr Arg Glu	Gln		
91		455		460		465
92	Asn Asp Lys Gly	Arg Glu Ser Lys Phe	Pro Tyr Ser Gly Ser	Ser		
93		470		475		480
94	Tyr Ser Arg Ser	Ser Tyr Thr Asp Ser	Ser Gln Gly Leu Ala	Gln		
95		485		490		495
96	His Ile His Ala	Leu Thr Leu Ser Pro	Ser Ala Ala His Thr	Leu		
97		500		505		510
98	Asp Leu Leu His	Asp His Pro His Pro	Pro Glu Glu Ala Glu	Ala		
99		515		520		525
100	Arg Ser Ala Met	Ile Val His Met Pro	Asp Leu Met Asp Ile	Ala		
101		530		535		540
102	His Ala Arg Ser	Arg Ser Pro Pro Tyr	Arg Arg Tyr Arg Ser	Arg		
103		545		550		555
104	Ser Arg Ser Pro	Pro Glu Phe Arg Gly	Gln Ser Pro Thr Lys	Arg		
105		560		565		570

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106	Asn	Val	Pro	Arg	Glu	Glu	Lys	Glu	Arg	Glu	Tyr	Phe	Asn	Arg	Tyr
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108	Arg	Glu	Val	Pro	Pro	Pro	Tyr	Asp	Ile	Lys	Ala	Tyr	Tyr	Gly	Arg
109					590					595					600
110	Ser	Val	Asp	Phe	Arg	Asp	Pro	Phe	Glu	Lys	Glu	Arg	Tyr	Arg	Glu
111					605					610					615
112	Trp	Glu	Arg	Lys	Tyr	Arg	Glu	Trp	Tyr	Glu	Lys	Tyr	Tyr	Lys	Gly
113					620					625					630
114	Tyr	Ala	Val	Gly	Ala	Gln	Pro	Arg	Pro	Ser	Ala	Asn	Arg	Glu	Asp
115					635					640					645
116	Phe	Ser	Pro	Glu	Arg	Leu	Leu	Pro	Leu	Asn	Ile	Arg	Asn	Ser	Pro
117					650					655					660
118	Phe	Thr	Arg	Gly	Arg	Arg	Glu	Asp	Tyr	Ala	Ala	Gly	Gln	Ser	His
119					665					670					675
120	Arg	Asn	Arg	Asn	Leu	Gly	Gly	Asn	Tyr	Pro	Glu	Lys	Leu	Ser	Thr
121					680					685					690
122	Arg	Asp	Ser	His	Asn	Ala	Lys	Asp	Asn	Pro	Lys	Ser	Lys	Glu	Lys
123					695					700					705
124	Glu	Ser	Glu	Asn	Val	Pro	Gly	Asp	Gly	Lys	Gly	Asn	Lys	His	Lys
125					710					715					720
126	Lys	His	Arg	Lys	Arg	Arg	Asn	Glu	Glu	Lys	Gly	Glu	Glu	Ser	Glu
127					725					730					735
128	Ser	Phe	Leu	Asn	Pro	Glu	Leu	Leu	Glu	Thr	Ser	Arg	Lys	Cys	Arg
129					740					745					750
130	Gly	Ser	Ser	Gly	Ile	Asp	Glu	Thr	Lys	Thr	Asp	Thr	Leu	Phe	Val
131					755					760					765
132	Leu	Pro	Ser	Arg	Asp	Asp	Ala	Thr	Pro	Val	Arg	Asp	Glu	Pro	Met
133					770					775					780
134	Asp	Ala	Glu	Ser	Ile	Thr	Phe	Lys	Ser	Val	Ser	Asp	Lys	Asp	Lys
135					785					790					795
136	Arg	Glu	Lys	Asp	Lys	Pro	Lys	Val	Lys	Ser	Asp	Lys	Thr	Lys	Arg
137					800					805					810
138	Lys	Ser	Asp	Gly	Ser	Ala	Thr	Ala	Lys	Lys	Asp	Asn	Val	Leu	Lys
139					815					820					825
140	Pro	Ser	Lys	Gly	Pro	Gln	Glu	Lys	Val	Asp	Gly	Asp	Arg	Glu	Lys
141					830					835					840
142	Ser	Pro	Arg	Ser	Glu	Pro	Pro	Leu	Lys	Lys	Ala	Lys	Glu	Glu	Ala
143					845					850					855
144	Thr	Lys	Ile	Asp	Ser	Val	Lys	Pro	Ser	Ser	Ser	Ser	Gln	Lys	Asp
145					860					865					870
146	Glu	Lys	Val	Thr	Gly	Thr	Pro	Arg	Lys	Ala	His	Ser	Lys	Ser	Ala
147					875					880					885
148	Lys	Asp	Thr	Arg	Arg	Gln	Ser	Gln	Pro	Arg	Thr	Arg	Arg	Ser	Lys
149					890					895					900
150	Arg	Thr	Val	Pro	Lys	Thr	Ser	Ser	Gln	Lys	Ser	Gln	Pro	Val	Arg
151					905					910					915
152	Thr	Arg	Arg	Pro	Arg	Ser	Leu	Arg	Lys	Ile	Asn	Tyr	Leu	Ile	Ala
153					920					925					930
154	Arg	Glu	Lys	Asn	Glu	Arg	Glu	Lys	Arg	Lys	Lys	Ser	Val	Asp	Lys

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155					935					940					945
156	Asp	Phe	Glu	Ser	Ser	Ser	Met	Lys	Ile	Ser	Lys	Val	Glu	Gly	Thr
157					950					955					960
158	Glu	Ile	Val	Lys	Pro	Ser	Pro	Lys	Arg	Lys	Met	Glu	Gly	Asp	Val
159					965					970					975
160	Glu	Lys	Leu	Glu	Arg	Thr	Pro	Glu	Lys	Asp	Lys	Ile	Ala	Ser	Ser
161					980					985					990
162	Thr	Thr	Pro	Ala	Lys	Lys	Ile	Lys	Leu	Asn	Arg	Glu	Thr	Gly	Lys
163					995					1000					1005
164	Lys	Ile	Gly	Asn	Ala	Glu	Asn	Ala	Ser	Thr	Thr	Lys	Glu	Pro	Ser
165					1010					1015					1020
166	Glu	Lys	Leu	Glu	Ser	Thr	Ser	Ser	Lys	Ile	Lys	Gln	Glu	Lys	Val
167					1025					1030					1035
168	Lys	Gly	Lys	Ala	Lys	Arg	Lys	Val	Ala	Gly	Ser	Glu	Gly	Ser	Ser
169					1040					1045					1050
170	Ser	Thr	Leu	Val	Asp	Tyr	Thr	Ser	Thr	Ser	Ser	Thr	Gly	Gly	Ser
171					1055					1060					1065
172	Pro	Val	Arg	Lys	Ser	Glu	Glu	Lys	Thr	Asp	Thr	Lys	Arg	Thr	Val
173					1070					1075					1080
174	Ile	Lys	Thr	Met	Glu	Glu	Tyr	Asn	Asn	Asp	Asn	Thr	Ala	Pro	Ala
175					1085					1090					1095
176	Glu	Asp	Val	Ile	Ile	Met	Ile	Gln	Val	Pro	Gln	Ser	Lys	Trp	Asp
177					1100					1105					1110
178	Lys	Asp	Asp	Phe	Glu	Ser	Glu	Glu	Glu	Asp	Val	Lys	Thr	Thr	Gln
179					1115					1120					1125
180	Pro	Ile	Gln	Ser	Val	Gly	Lys	Pro	Ser	Ser	Ile	Ile	Lys	Asn	Val
181					1130					1135					1140
182	Thr	Thr	Lys	Pro	Ser	Ala	Thr	Ala	Lys	Tyr	Thr	Glu	Lys	Glu	Ser
183					1145					1150					1155
184	Glu	Gln	Pro	Glu	Lys	Leu	Gln	Lys	Leu	Pro	Lys	Glu	Ala	Ser	His
185					1160					1165					1170
186	Glu	Leu	Met	Gln	His	Glu	Leu	Arg	Ser	Ser	Lys	Gly	Ser	Ala	Ser
187					1175					1180					1185
188	Ser	Glu	Lys	Gly	Arg	Ala	Lys	Asp	Arg	Glu	His	Ser	Gly	Ser	Glu
189					1190					1195					1200
190	Lys	Asp	Asn	Pro	Asp	Lys	Arg	Lys	Ser	Gly	Ala	Gln	Pro	Asp	Lys
191					1205					1210					1215
192	Glu	Ser	Thr	Val	Asp	Arg	Leu	Ser	Glu	Gln	Gly	His	Phe	Lys	Thr
193					1220					1225					1230
194	Leu	Ser	Gln	Ser	Ser	Lys	Glu	Thr	Arg	Thr	Ser	Glu	Lys	His	Glu
195					1235					1240					1245
196	Ser	Val	Arg	Gly	Ser	Ser	Asn	Lys	Asp	Phe	Thr	Pro	Gly	Arg	Asp
197					1250					1255					1260
198	Lys	Lys	Val	Asp	Tyr	Asp	Ser	Arg	Asp	Tyr	Ser	Ser	Ser	Lys	Arg
199					1265					1270					1275
200	Arg	Asp	Glu	Arg	Gly	Glu	Leu	Ala	Arg	Arg	Lys	Asp	Ser	Pro	Pro
201					1280					1285					1290
202	Arg	Gly	Lys	Glu	Ser	Leu	Ser	Gly	Gln	Lys	Ser	Lys	Leu	Arg	Glu
203					1295					1300					1305

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204 Glu Arg Asp Leu Pro Lys Lys Gly Ala Glu Ser Lys Lys Ser Asn
 205 1310 1315 1320
 206 Ser Ser Pro Pro Arg Asp Lys Lys Pro His Asp His Lys Ala Pro
 207 1325 1330 1335
 208 Tyr Glu Thr Lys Arg Pro Cys Glu Glu Thr Lys Pro Val Asp Lys
 209 1340 1345 1350
 210 Asn Ser Gly Lys Glu Arg Glu Lys His Ala Ala Glu Ala Arg Asn
 211 1355 1360 1365
 212 Gly Lys Glu Ser Ser Gly Ala Asn Cys His Val Tyr Leu Thr Arg
 213 1370 1375 1380
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219 <210> SEQ ID NO: 2

220 <211> LENGTH: 5173

221 <212> TYPE: DNA

222 <213> ORGANISM: Unknown

224 <220> FEATURE:

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227 <223> OTHER INFORMATION: P2P cDNA

229 <400> SEQUENCE: 2

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 232 ggaattccta gaagttttat gatggaagtg aaagatccta acatgaaagg tgcaatgctt 180
 233 accaactctg gaaaatatgc aataccaact atagatgcag aggcctatgc aatcgggaag 240
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 235 atcccagcag agctcttgtg cctcatctgc aaagacatca tgactgatgc tgtgggtcatt 360
 236 ccctgctgtg gaaacagttc atgtgatgaa tgtataagaa cgacactctt ggagtcagat 420
 237 aaacatacat gtccaacatg tcacaaaaat gatgtttctc ctgatgcttt aattgccaac 480
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 256 ccctatagtg ggtcatcgta ttcaagaagt tcatacactg actcaagtca aggtctggct 1620

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